



## Pulmonary Tuberculosis Conversion Documented by Microscopic Staining for Detection of Dynamic, Dormant, and Dead Mycobacteria (DDD Staining)

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Detecting the infectiousness of *Mycobacterium tuberculosis* mycobacteria in the sputum specimens collected from patients with pulmonary tuberculosis remains cumbersome. Sputum may contain contagious dormant and dynamic mycobacteria along with noncontagious, dead mycobacteria (1, 2, 3). Routine microscopy after auramine or Ziehl-Neelsen staining misses dormant mycobacteria (4, 5), whose detection requires a specific microscopy protocol (5, 6). Additional specific protocols are required for detecting live/dead (7) or metabolically active/inactive *M. tuberculosis* mycobacteria (1). As reported here, we have set up a protocol for the one-shot microscopy detection of dynamic, dormant, and dead mycobacteria—hence, the acronym "DDD" that we gave to this protocol. The DDD protocol incorporates 4',6-diamidino-2-phenylindole (DAPI) staining of all mycobacteria, fluorescein-di-acetate (FDA) staining of dynamic mycobacteria (8, 9, 10, 11), and Nile red (NR) staining of dormant mycobacteria (see the supplemental material) (5, 6).

As a proof of concept, the DDD protocol was used to monitor the changes in M. tuberculosis mycobacteria in sputum specimens collected from one patient treated for pulmonary tuberculosis. A 33-year-old woman with a medical history of community-acquired pneumonia at the age of 15 years was diagnosed in August 2017 with pulmonary tuberculosis. Acid-fast bacilli observed in a sputum smear after Ziehl-Neelsen staining, identified as rifampin-susceptible M. tuberculosis by real-time PCR, grew in a solid culture medium (12). The patient benefited from standard antituberculous treatment associating oral ethambutol, pyrazinamide, isoniazid, and rifampin. The clinical course was favorable and rifampin blood dosages confirmed the patient's adherence to therapy (serum peak concentration,  $8 \mu g/ml$ ), but continuous observation of acid-fast bacilli over 6 weeks brought into question the contagiousness of the patient.

Of 133 mycobacteria observed by DDD staining in three Ziehl-Neelsen-positive, culture-positive sputum specimens collected before treatment, 92 (69.2%) were dynamic mycobacteria, 33 (24.8%) were dead mycobacteria, and 8 (6%) were dormant mycobacteria, staining DAPI positive and either FDA positive or FDA negative (Fig. 1A to C). Of 159 mycobacteria observed by DDD staining in three Ziehl-Neelsen-positive, culture-negative sputum specimens collected 24 to 60 days after the initiation of the antituberculous treatment, 47 (29%) were dynamic, 88 (55.5%) dead, and 24 (15.5%) dormant, the cell lengths of which were up to 4.4  $\mu$ m (Fig. 1A and D). No bacilli were observed after DDD staining of one negative-control decontaminated sputum sample.

The significant decrease in mycobacterial vitality measured by DDD staining after treatment (P < 0.001) correlated with a favorable clinical course and sputum conver-

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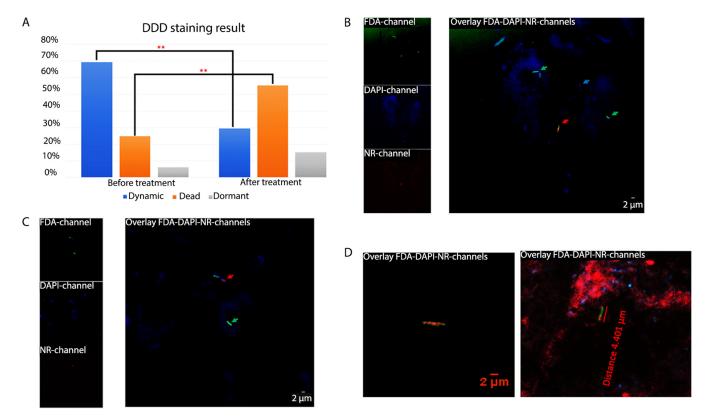
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**FIG 1** DDD staining results after microscopic observation and counting. DAPI, FDA, and NR channels were used for the microscopic acquisition and image overlay. Image acquisition was performed with a Zeiss spinning-disk confocal microscope using a  $63 \times$ , 1.4 numeric aperture (NA) oil immersion objective. (A) Comparison between the percentages of dynamic, dead, and dormant *Mycobacterium tuberculosis* mycobacteria in the sputum specimens collected before and after antituberculous treatment. \*\*, P < 0.001 by Pearson's chi-square statistic test. (B) Fluorescence microscopy images of sputum smears collected before antituberculous treatment showing dynamic mycobacteria as FDA- and DAPI-positive bacilli (green arrows), dead mycobacteria as DAPI-positive and FDA-negative bacilli (blue arrow), and dormant mycobacterium as FDA- and DAPI-positive bacilli holding NR-positive intracellular inclusions (red arrow). (C) Fluorescence microscopy images of sputum smears from specimens collected before antituberculous treatment, showing dynamic mycobacteria as FDA- and DAPI-positive bacilli (green arrow) and a dormant mycobacterium as FDA-negative and DAPI-positive bacilli with NR-positive intracellular lipid bodies (red arrow). (D) Fluorescence microscopy images of sputum smears from specimens collected after antituberculous treatment, showing a dormant *M. tuberculosis* bacterium holding five NR-positive intracellular inclusions and a dormant *M. tuberculosis* bacterium measuring 4.4 μm and containing 2 lipid bodies.

sion, as previously reported (7, 8). And yet, the percentages of dormant mycobacteria before and after treatment did not differ significantly (Fig. 1A), suggesting that dormant mycobacteria are not susceptible to antituberculous treatment, in line with a previous observation that an increasing percentage of lipidic-inclusion-positive bacilli in sputum after three to four weeks of antituberculous treatment correlated with an unfavorable outcome (13).

The DDD protocol could be applied to paired sputum specimens collected from patients responding poorly to the antituberculous treatment to precisely determine the infectiousness of such patients. The DDD protocol can be used on fresh and  $-80^{\circ}$ C-stored sputum specimens that are alcohol inactivated after DDD staining to protect laboratory workers from exposure to viable mycobacteria. From this perspective, we are now considering automatizing the DDD detection by either using a recently developed scanner protocol or coupling it with flow cytometry (14).

This study was approved by the Ethics Committee of Institut Fédératif de Recherche 48, Marseille, France.

## **SUPPLEMENTAL MATERIAL**

Supplemental material for this article may be found at https://doi.org/10.1128/JCM 01108-18

SUPPLEMENTAL FILE 1, PDF file, 0.2 MB.

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